In The Claims:

1. (previously presented) A method for detecting a target sequence, comprising:
   a) providing:
      i) a sample suspected of containing said target sequence;
      ii) oligonucleotides capable of forming an invasive cleavage structure in the presence of said target sequence; and
      iii) an agent for detecting the presence of an invasive cleavage structure; and
   b) exposing said sample to said oligonucleotides and said agent under conditions such that said invasive cleavage structure is cleaved by said agent; and
   c) detecting the cleavage of said invasive cleavage structure, thereby detecting said target sequence.

2. (original) The method of Claim 1, wherein said agent comprises a cleavage agent.

3. (previously presented) The method of Claim 2, wherein said exposing said sample to said oligonucleotides and said cleavage agent comprises exposing said sample to said oligonucleotides and said cleavage agent under conditions wherein an invasive cleavage structure is formed between said target sequence and said oligonucleotides if said target sequence is present in said sample, wherein said invasive cleavage structure is cleaved by said cleavage agent to form a cleavage product.

4. (cancelled)

5. (previously presented) The method of Claim 1, wherein said target sequence comprises a first region and a second region, said second region downstream of and contiguous to said first region, and wherein said oligonucleotides comprise

first and second oligonucleotides, wherein at least a portion of said first oligonucleotide is completely complementary to said first region of said target sequence and wherein said second oligonucleotide comprises a 3' portion and a 5' portion, wherein said 5' portion is completely complementary to said second region of said target sequence.

6. (original) The method of Claim 1, wherein said target sequence is selected from the group consisting of human cytomegalovirus viral DNA; polymorphisms in human apolipoprotein E gene; mutations in human hemochromatosis gene; mutations in human MTHFR; prothrombin 20210GA polymorphism; HR-2 mutation in human factor V gene; single nucleotide polymorphisms in human TNF-a gene, and Leiden mutation in human factor V gene.

7. (original) A kit for detecting a target sequence comprising oligonucleotides capable of forming an invasive cleavage structure in the presence of said target sequence.

8. (original) The kit of Claim 7, further comprising an agent for detecting the presence of an invasive cleavage structure.

9. (original) The kit of Claim 8, wherein said agent comprises a cleavage agent.

10. (previously presented) The kit of Claim 7, wherein said oligonucleotides comprise first and second oligonucleotides, said first oligonucleotide comprising a 5' portion complementary to a first region of said target sequence and said second oligonucleotide comprising a 3' portion and a 5' portion, said 5' portion complementary to a second region of said target sequence downstream of and contiguous to said first region of said target sequence.

11. (original) The kit of Claim 7, wherein said target sequence is selected from the group consisting of human cytomegalovirus viral DNA; polymorphisms in human

apolipoprotein E gene; mutations in human hemochromatosis gene; mutations in human MTHFR; prothrombin 20210GA polymorphism; HR-2 mutation in human factor V gene; single nucleotide polymorphisms in human TNF-a gene, and Leiden mutation in human factor V gene.